

AMENDMENT

In the Claims

Please amend the claims without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents as follows.

1-45. (Canceled)

46. (Previously Presented) An isolated polynucleotide consisting of 30 contiguous nucleotides of SEQ ID No. 1 or the complement thereof.

47. (Previously Presented) An isolated polynucleotide consisting of SEQ ID No. 3 or the complement of SEQ ID No. 3.

48. (Previously Presented) An isolated polynucleotide consisting of SEQ ID No. 4 or the complement of SEQ ID No. 4.

49. (Previously Presented) An isolated polynucleotide consisting of SEQ ID No. 5 or the complement of SEQ ID No. 5.

50. (Previously Presented) An isolated polynucleotide consisting of SEQ ID No. 1 or the complement of SEQ ID No. 1.

51. (Canceled)

52-54. (Canceled)

55. (Currently Amended) An isolated polynucleotide ~~consisting of comprising~~ the polynucleotide of any one of claims 46-50 and optionally a moiety that produces a signal or a binding site for a moiety that produces a signal when the polynucleotide hybridizes to *Pseudomonas* DNA.

56. (Previously Presented) A kit for detecting *Pseudomonas*, comprising one or more isolated polynucleotide(s) selected from the group consisting of SEQ ID No. 3, SEQ ID No. 4, SEQ ID No. 5, SEQ ID No. 1, 30 contiguous nucleotides of SEQ ID No. 1, and the complements thereof.

57. (Canceled)

58. (Currently Amended) A method for detecting *Pseudomonas* in a sample, the method comprising the steps of determining if

(a) contacting the sample with a first polynucleotide comprising 10 to ~~250~~ or more contiguous nucleotides of SEQ ID No. 1, or the complement of SEQ ID No. 1; wherein the polynucleotide is 10-250 nucleotides long,

(b) hybridises-hybridizing said polynucleotide to *Pseudomonas* DNA in the sample, thereby detecting wherein hybridization detects *Pseudomonas* in the sample, if hybridisation occurs.

59. (Currently Amended) A method for detecting *Pseudomonas* in a sample, the method comprising amplifying *Pseudomonas* DNA in the sample using a first polynucleotide comprising 10 to ~~250~~ or more contiguous nucleotides of SEQ ID No. 1, or the complement of SEQ ID No. 1, wherein the first polynucleotide is 10-250 nucleotides long—and a second polynucleotide comprising 10 to ~~250~~ or more contiguous nucleotides of i) SEQ ID No. 1, ii) the complement of SEQ ID No. 1, iii) the 23S gene, or iv) the 5S gene, wherein the second polynucleotide is 10-250 nucleotides long, thereby detecting *Pseudomonas* in the sample if amplification occurs.

60. (Previously Presented) A method for detecting *Pseudomonas* in a sample, the method comprising amplifying *Pseudomonas* DNA using a first polynucleotide and a second polynucleotide, wherein the first polynucleotide is SEQ ID No. 3 or SEQ ID No. 5 and the second polynucleotide is SEQ ID No. 2, thereby detecting *Pseudomonas* in the sample if amplification occurs.

61. (Previously Presented) The method of claim 58 wherein the first polynucleotide further comprises a moiety that produces a signal or a binding site for a moiety that produces a signal when the polynucleotide hybridizes to *Pseudomonas* DNA.

62. (Previously Presented) The method of any one of claims 58-60, wherein the *Pseudomonas* is *Pseudomonas aeruginosa*.

63. (Previously Presented) The method of claim 58 wherein the first polynucleotide differentially hybridizes to DNA from different strains or species of *Pseudomonas*.

64. (Previously Presented) The method of claim 59 or 60 wherein the second polynucleotide differentially hybridizes to DNA from different strains or species of *Pseudomonas*.

65. (Previously Presented) A kit for detecting *Pseudomonas*, comprising the polynucleotide of claim 55.

66. (Currently Amended) The ~~method-kit~~ of claim 56, wherein the ~~primer or probe polynucleotide~~ is SEQ ID NO:4.

67. (Previously Presented) The method of claim 58 or 59, wherein the first polynucleotide comprises 15 to 30 contiguous nucleotides of SEQ ID No. 1, or the complement of SEQ ID No. 1.

68. (Currently Amended) A method for producing a primer or probe for detecting the presence of one or more *Pseudomonas* strain(s) that are to be detected in a sample, wherein the method comprises:

a) ~~comparing performing a sequence alignment and sequence comparison to identify differences between~~ the sequence of the 23S/5S intergenic region of genomic DNA isolated from one or more *Pseudomonas* strain(s) that are to be detected ~~with-and~~ the sequence of the 23S/5S

intergenic region of genomic DNA isolated from one or more *Pseudomonas* strain(s) that are not to be detected; and

b) producing a nucleic acid primer or probe comprising selecting a nucleic acid sequence of at least 15 contiguous nucleotides of SEQ ID NO:1, wherein the at least 15 contiguous nucleotides differ that differs in at least one nucleotide position between the sequence of the 23S/5S intergenic region of the *Pseudomonas* strain(s) that are to be detected and the sequence of the 23S/5S intergenic region of the *Pseudomonas* strain(s) that are not to be detected, wherein the at least 15 contiguous nucleotides can be used as a primer or probe can be used for detecting the presence of the one or more *Pseudomonas* strain(s) that are to be detected.

69. (Previously Presented) The method of claim 68, wherein the 23S/5S intergenic region of genomic DNA has the sequence of SEQ ID NO:1.

70. (Previously Presented) The method of claim 68, wherein the 23S/5S intergenic region of genomic DNA has a sequence that is at least 90% homologous to SEQ ID NO:1.

71. (Previously Presented) The method of claim 68, wherein the 23S/5S intergenic region of genomic DNA comprises SEQ ID NO:5.

72. (Previously Presented) The method of claim 68, wherein the primer or probe comprises SEQ ID NO:3.

73. (Previously Presented) The method of claim 68, wherein the primer or probe comprises SEQ ID NO:4.

74. (Previously Presented) The method of claim 68, wherein the nucleic acid sequence of b) is at least 30 contiguous nucleotides.

75. (Currently Amended) The method of claim 68, wherein the nucleic acid sequence of b) is at least 15-250 contiguous nucleotides.

76. (Previously Presented) The method of claim 68, wherein the nucleic acid sequence of b) is DNA.

77. (Previously Presented) The method of claim 68, wherein the nucleic acid sequence of b) is RNA.

78. (Previously Presented) The method of claim 68, wherein the nucleic acid sequence of b) is PNA.